

Figure 1. RT-PCR analysis of barley limit dextrinase inhibitor expression.

Figure 2. Northern blot analysis of limit dextrinase expression.

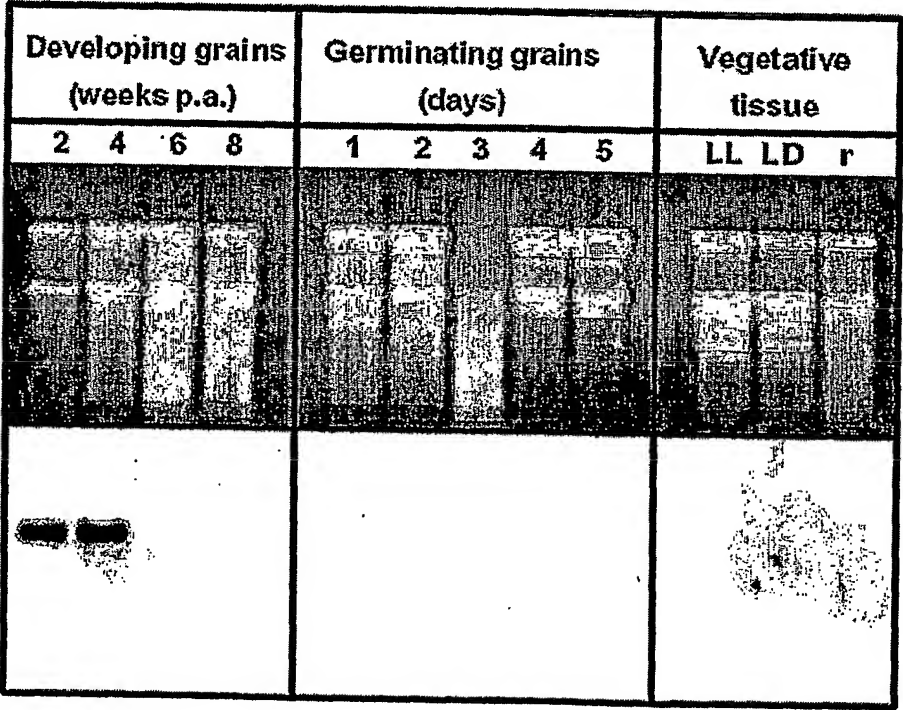


Figure 3. Southern blot analysis of limit dextrinase inhibitor in barley genomic DNA.

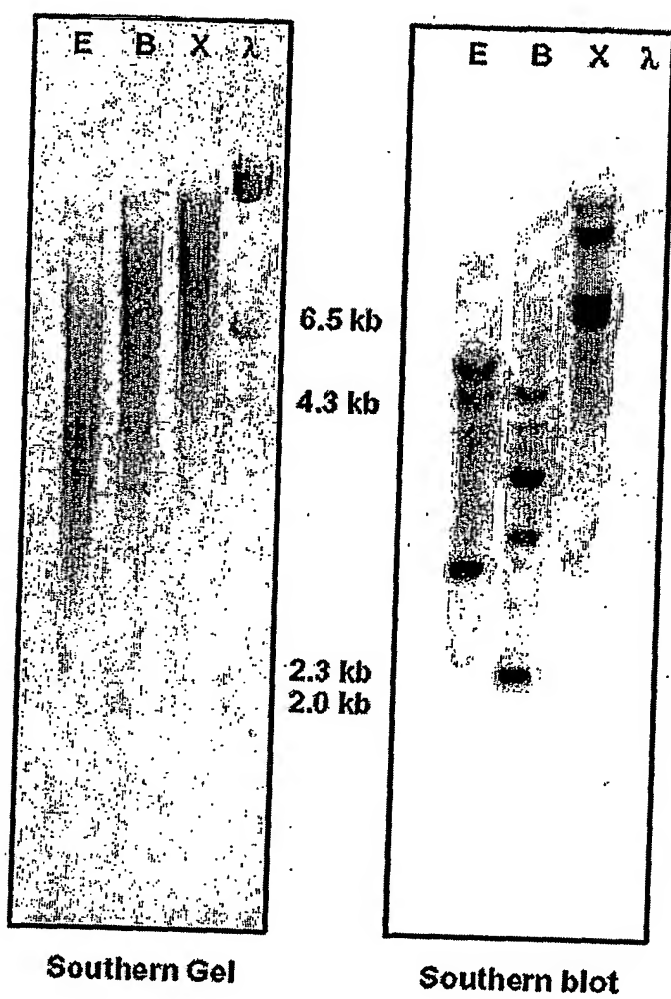


Figure 4. Isolation of limit dextrinase inhibitor promoter fragments by genome walking PCR.

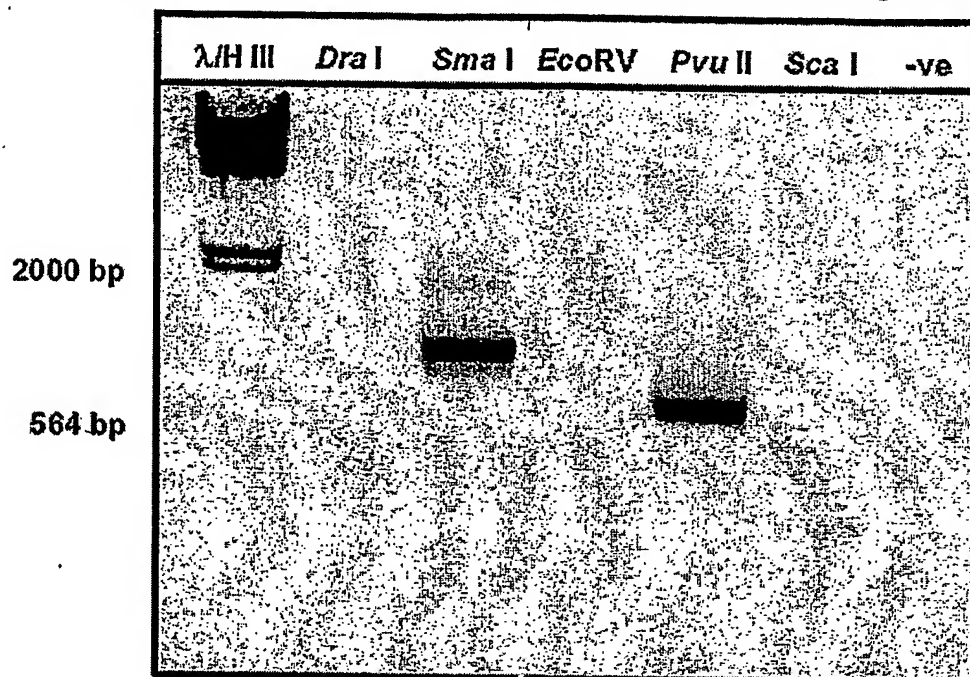
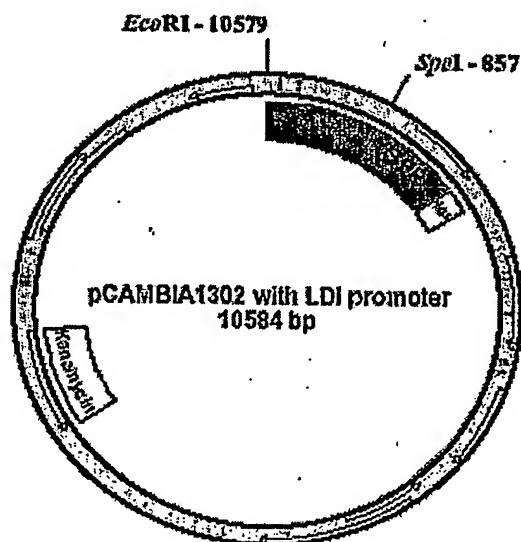
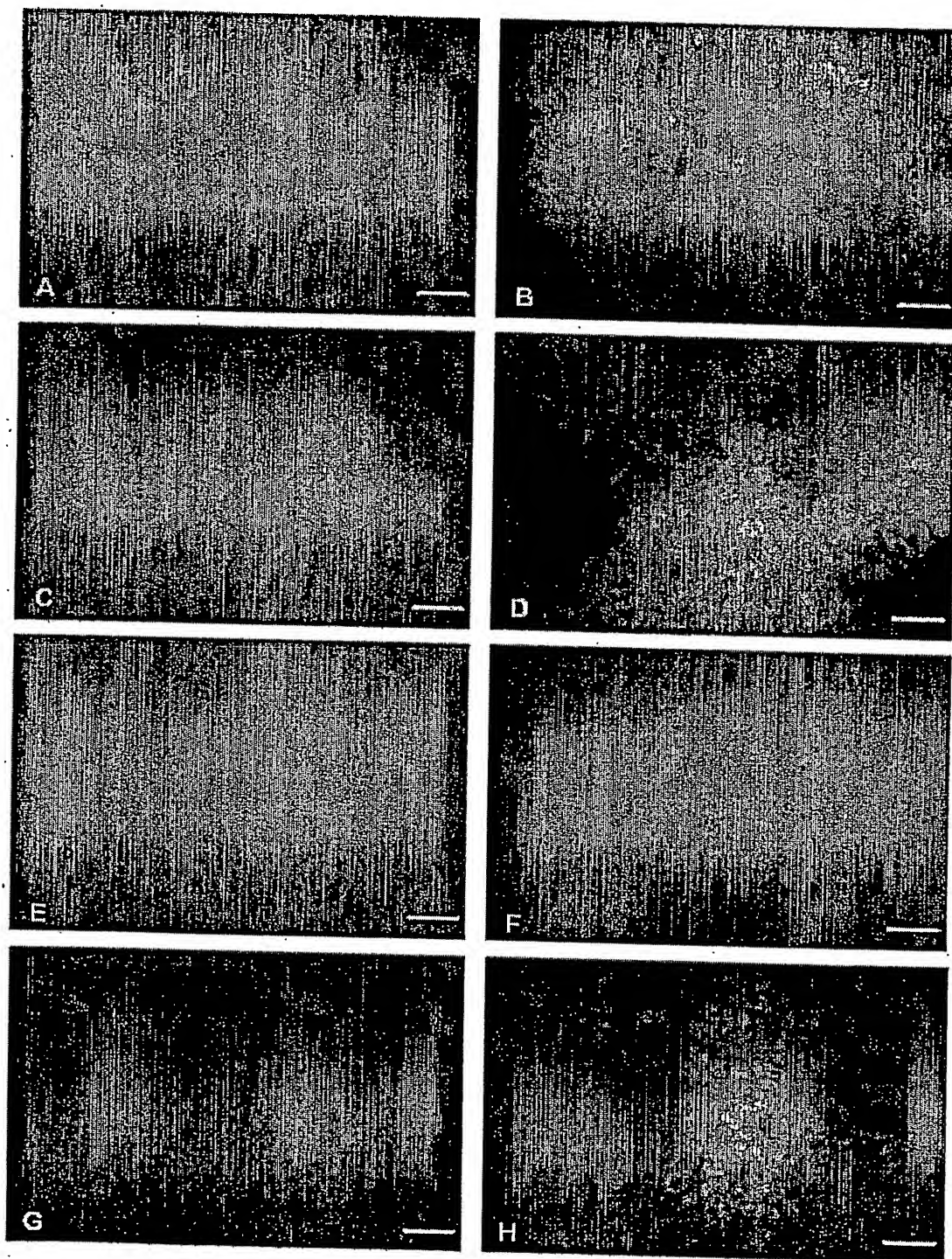


Figure 5. Barley transformation construct containing the limit dextrinase inhibitor promoter.



4/21

Figure 6. Transient expression assays using the limit dextrinase promoter: GFP construct.



5/21

Figure 7.

Start	End	Score	Promoter Sequence
247	297	0.89	ATGCCCCGTGTAAAAGAAACCCCTTCTTTCCTAAAAATATA A TATCATCGT
273	323	0.95	TTTCCTAAAAATATATATCATCGTCCGTCATGATACGTTT A TGTATTCAA
652	702	0.83	CAAGAACCTCCAAATAAACGCCAACAAGAAAGAAATGAGC A TTACTTGCG

6/21

Figure 8

Sequences producing significant alignments:			Score (bits)	E Value
gi 18868 emb X13443.1 HVAATI	Barley mRNA for alpha-amylase/...		82	2e-12
gi 22035404 gb AY124482.1	Danio rerio myogenin gene, exons...		80	6e-12
gi 24614584 gb AY050653.1	Giardia intestinalis SEC24 (SEC2...		76	1e-10
gi 10938038 gb AF162890.1	AF162890S1 Mus musculus peroxisom...		76	1e-10
gi 5821237 dbj AB021922.1	Homo sapiens gene for lectin-lik...		76	1e-10
gi 3721562 dbj AB011276.1	Mus musculus gene for alphaal ca...		74	4e-10
gi 30313388 gb AY099112.1	Rattus norvegicus obese protein ...		72	2e-09
gi 18140057 gb AF457660.1	Castanea dentata clone ACS2 vasc...		72	2e-09
gi 4104807 gb AF039526.1	AF039526 Homo sapiens MHC class I ...		72	2e-09
gi 8050595 gb AF233737.1	AF233737 Agrotis ipsilon Aic5 chym...		72	2e-09
gi 6690643 gb AF191544.1	AF191544 Homo sapiens estrogen rec...		72	2e-09
gi 6164589 gb AF051769.1	AF051769 Homo sapiens hyaluronidas...		72	2e-09
gi 3643823 gb AF075270.1	AF075270 Hordeum vulgare high affi...		72	2e-09
gi 19919401 gb AF435445.1	Pleurotus ostreatus manganese pe...		70	6e-09
gi 8132114 gb AF153014.1	Trichomonas vaginalis Tvp14 (tvp1...		70	6e-09
gi 4456992 gb AF077743.1	AF077743 Mus musculus transcriptio...		70	6e-09
gi 12276207 gb AF269146.1	AF269146 Bilophila wadsworthia ta...		70	6e-09
gi 14275833 emb AJ289605.1	MMU289605 Mus musculus partial L...		70	6e-09
gi 3378604 emb AJ009889.1	HSAJ9889 Homo sapiens GHR gene, V...		70	6e-09
gi 3916231 gb AF074397.1	AF074397 Homo sapiens anti-mulleri...		70	6e-09
gi 5139506 emb Z18892.2	MMDESMINP Mus musculus desmin gene		70	6e-09
gi 15487305 dbj AB060299.1	Mus musculus gene for acetyl Co...		70	6e-09
gi 12697590 dbj AB046716.1	Homo sapiens hST3Gal I gene for...		70	6e-09
gi 25453365 gb AY050651.2	Giardia intestinalis MYB (MYB) m...		68	2e-08
gi 13183059 gb AF237414.1	Anaplasma phagocytophilum RNA po...		68	2e-08
gi 13625520 gb AY014277.1	Lolium perenne gibberellin 20-ox...		68	2e-08
gi 17105179 gb AF439558.1	AF439558 Mus musculus X2CR1 gene,...		68	2e-08
gi 16209547 gb AY052528.1	Glycine max calmodulin isoform-4...		68	2e-08
gi 15213480 gb AF241535.1	AF241535 Homo sapiens mucin 4 (MU...		68	2e-08
gi 15558849 emb AJ310936.1	FSO310936 Fusarium solani chy ge...		68	2e-08
gi 4878023 gb AF131239.2	AF131239 Rattus norvegicus alpha 1...		68	2e-08
gi 15216031 emb AJ318812.1	VFA318812 Vicia faba var. minor ...		68	2e-08
gi 4454294 emb AJ132779.1	MMU132779 Mus musculus p107 gene ...		68	2e-08
gi 3133088 emb Y16736.1	HSA16736 Homo sapiens dif-2 gene, p...		68	2e-08
gi 6690521 gb AF154245.1	AF154245 Rattus norvegicus chemota...		68	2e-08
gi 5731977 gb AF114032.1	AF114032 Mus musculus glycogenin-1...		68	2e-08
gi 26453412 dbj AB094665.1	Seriola quinqueradiata YGHL1 ge...		68	2e-08
gi 4039145 gb AF099083.1	AF099083 Homo sapiens growth hormo...		68	2e-08
gi 2739123 gb AF029214.1	MMOX2S1 Mus musculus MRC OX-2 anti...		68	2e-08
gi 2895903 gb AF046916.1	AF046916 Ruminococcus flavefaciens...		68	2e-08
gi 1916583 gb U53907.1	RNU53907 Rattus norvegicus microsate...		68	2e-08

7/21

gi 6683556 dbj AB024534.1	Rattus norvegicus gene for thiaz...	68	2e-08
gi 7109286 gb AF227508.1	Rattus norvegicus intestinal alka...	66	1e-07
gi 13345792 gb AF332759.1	Homo sapiens partially duplicate...	66	1e-07
gi 5002511 emb Z98266.1 HSZ98266	Homo sapiens gene encoding...	66	1e-07
gi 6560627 gb AF112228.1 HSCD30P1	Homo sapiens CD30 protein...	66	1e-07
gi 24475537 dbj AB084484.1	Betula platyphylla DNA, microsa...	66	1e-07
gi 28875405 gb AF515463.1	Biomphalaria glabrata fibrinogen...	64	4e-07
gi 18140058 gb AF457661.1	Castanea dentata clone ACS10A va...	64	4e-07
gi 2581766 gb U77633.1 RNU77633	Rattus norvegicus chromosom...	64	4e-07
gi 2764739 emb AJ002743.1 HSAJ2743	Homo sapiens cardiotox...	64	4e-07
gi 7579914 emb AJ277249.1 HSA277249	Homo sapiens partial HR...	64	4e-07
gi 1518845 gb U63899.1 MMU63899	Mus musculus Girk2 gene, pr...	64	4e-07
gi 7109284 gb AF227507.1	Rattus norvegicus intestinal alka...	62	2e-06
gi 12744733 gb AF318503.1	Danio rerio Myod (myod) gene, co...	60	6e-06
gi 2581767 gb U77634.1 RNU77634	Rattus norvegicus chromosom...	60	6e-06
gi 14251200 gb AF220499.2 AF220499	Acidithiobacillus ferroo...	60	6e-06
gi 14043019 gb AF221946.2 AF221946	Rickettsia rickettsii ce...	60	6e-06
gi 2342636 emb Y11638.1 MMY11638	M.musculus CYP4A14 gene, e...	60	6e-06
gi 18873678 emb AJ272507.1 HSA272507	Homo sapiens partial K...	60	6e-06
gi 2564335 dbj AB008218.1 AB008218S1	Homo sapiens gene for ...	60	6e-06
gi 17907575 emb AJ409277.1 CDR409277	Camelus dromedarius pa...	58	2e-05
gi 5091690 gb AF139181.1 AF139181	Bartonella henselae S-ade...	58	2e-05
gi 14164368 dbj AB052355.1 AB05234S16	Mus musculus gene for...	58	2e-05
gi 15081477 gb AF401090.1	Wolbachia pipientis RNA polymera...	56	9e-05
gi 17298240 gb AF283339.1 F283327S13	Homo sapiens candidate...	56	9e-05
gi 4139055 gb AF072833.1 AF072833	Homo sapiens SP23 gene, p...	56	9e-05
gi 17298258 gb AF283357.1 F283327S31	Homo sapiens candidate...	54	4e-04
gi 18413572 emb AJ428930.1 XLA428930	Xenopus laevis partial...	54	4e-04
gi 18873687 emb AJ272516.1 HSA272516	Homo sapiens partial K...	54	4e-04
gi 29648446 gb AY190007.1	Pan paniscus clone BoE26-M13R LI...	52	0.001
gi 22651882 gb AF291761.1	Ipomoea batatas S-adenosylmethio...	52	0.001
gi 22347797 gb AF532732.1	Danio rerio mx gene, promoter se...	52	0.001
gi 11230634 emb AJ289159.1 HSA289159	Homo sapiens CD30 gene...	52	0.001
gi 3342093 gb AF074905.1 HOMOSLC04	Homo sapiens neuronal an...	50	0.006
gi 13377504 gb AF325198.1 AF325198	Triticum aestivum LRR14 ...	48	0.023
gi 6649909 gb AF026274.1 AF026274	Mus musculus Sumiko (sumi...	48	0.023
gi 6224791 gb AF190816.1 AF190816	Homo sapiens complement f...	48	0.023
gi 4104439 gb AF035664.1 HSTGFRBI3	Homo sapiens transformin...	48	0.023
gi 21213045 emb AJ487974.1 EAM487974	Enterobacter amnigenus...	48	0.023
gi 15638904 gb AC024246.8	Homo sapiens BAC clone RP11-6430...	46	0.090
gi 15638822 gb AC079120.6	Homo sapiens BAC clone RP11-345M...	46	0.090
gi 13793999 gb AY029002.1	Pinus taeda isolate PTLTP3-iii27...	46	0.090
gi 11093799 gb AF285184.1 AF285184	Mus musculus basic trans...	46	0.090
gi 2984654 gb AF039088.1 AF039088	Homo sapiens non-hepatic ...	46	0.090
gi 3342092 gb AF074904.1 HOMOSLC03	Homo sapiens neuronal an...	44	0.36
gi 29029467 gb AY173030.1	Danio rerio zinc finger transcri...	44	0.36

8/21

gi 2281684 gb AF009433.1 AH006708S06	Homo sapiens clone 22 ...	44	0.36
gi 13936217 gb AY029021.1	Pinus radiata isolate PRLTP3-iii...	44	0.36
gi 13936206 gb AY029014.1	Pinus taeda isolate PTLTP9-iii15...	44	0.36
gi 13936204 gb AY029013.1	Pinus taeda isolate PTLTP4-i360 ...	44	0.36
gi 13794006 gb AY029007.1	Pinus taeda isolate PTLTP3-v94 n...	44	0.36
gi 13794003 gb AY029005.1	Pinus taeda isolate PTLTP6-i425 ...	44	0.36
gi 24210408 emb AJ320160.1 FNU320160	Fusobacterium nucleatu...	44	0.36
gi 13928026 emb AL121594.6 CNS01DRY	Human chromosome 14 DNA...	44	0.36
gi 8191116 gb AC040163.3 AC040163	Homo sapiens chromosome 1...	44	0.36
gi 6707080 gb AF139182.1 AF139182	Bartonella henselae filam...	44	0.36
gi 4028938 gb AC004230.1 AC004230	Homo sapiens Chromosome 1...	44	0.36
gi 21623971 dbj AP001094.6	Homo sapiens genomic DNA, chrom...	44	0.36
gi 19879812 dbj AP001363.4	Homo sapiens genomic DNA, chrom...	44	0.36

Alignments

>gi|18868|emb|X13443.1|HVAATI Barley mRNA for alpha-amylase/trypsin
inhibitor
Length = 672

Score = 81.8 bits (41), Expect = 2e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

Query: 793 aagagattgaaccaacgaccaataaaactagtagtcaacaatg 833
 |||||
Sbjct: 1 aagagattgaaccaacgaccaataaaactagtagtcaacaatg 41

>gi|22035404|gb|AY124482.1| Danio rerio myogenin gene, exons 1, 2 and 3
and complete cds
Length = 4260

Score = 79.8 bits (40), Expect = 6e-12
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 3 tcgattactatagggcacgcgtgggtcgacggcccggtg 42
 |||||
Sbjct: 4246 tcgattactatagggcacgcgtgggtcgacggcccggtg 4207.

>gi|24614584|gb|AY050653.1| Giardia intestinalis SEC24 (SEC24) mRNA,
complete cds
Length = 1420

Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Minus

Query: 5 gattactatagggcacgcgtgggtcgacggcccggtg 42
 |||||
Sbjct: 1417 gattactatagggcacgcgtgggtcgacggcccggtg 1380

9/21

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 23 actatagggcacgcgtgggtcgacggcccgggctg 56

>gi|10938038|gb|AF162890.1|AF162890S1 Mus musculus peroxisomal assembly
protein PEX3P (Pex3) gene,
promoter and exon 1
Length = 2785

Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Plus

Query: 5 gattactatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 13 gattactatagggcacgcgtgggtcgacggcccgggctg 50

>gi|5821237|dbj|AB021922.1| Homo sapiens gene for lectin-like oxidized LDL
receptor, promoter
region
Length = 2463

Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Plus

Query: 5 gattactatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 13 gattactatagggcacgcgtgggtcgacggcccgggctg 50

>gi|3721562|dbj|AB011276.1| Mus musculus gene for alpha calcium
channel, partial cds
Length = 2099

Score = 73.8 bits (37), Expect = 4e-10
Identities = 40/41 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctgttattgg 49
 |||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctgttattgg 41

10/21

>gi|30313388|gb|AY099112.1| Rattus norvegicus obese protein gene, 5'
flanking region and
partial cds
Length = 1127

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtggtcgacggcccgggctg 42
|||||
Sbjct: 17 ttactatagggcacgcgtggtcgacggcccgggctg 52

>gi|18140057|gb|AF457660.1| Castanea dentata clone ACS2 vascular protein
gene, promoter
region
Length = 685

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtggtcgacggcccgggctg 42
|||||
Sbjct: 9 ttactatagggcacgcgtggtcgacggcccgggctg 44

>gi|4104807|gb|AF039526.1|AF039526 Homo sapiens MHC class I related protein
1 (MR1) gene, partial
cds
Length = 1423

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtggtcgacggcccgggctg 42
|||||
Sbjct: 4 ttactatagggcacgcgtggtcgacggcccgggctg 39

>gi|8050595|gb|AF233737.1|AF233737 Agrotis ipsilon AiC5 chymotrypsinogen
gene, promoter region
Length = 951

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtggtcgacggcccgggctg 42
|||||
Sbjct: 11 ttactatagggcacgcgtggtcgacggcccgggctg 46

11/21

>gi|6690643|gb|AF191544.1|AF191544 Homo sapiens estrogen receptor beta
gene, promoter region and
partial cds
Length = 2495

Score = 71.9 bits (36), Expect = 2e-09
Identities = 39/40 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccggtgttattg 48
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccggtgttattg 40

>gi|6164589|gb|AF051769.1|AF051769 Homo sapiens hyaluronidase-like
pseudogene 1 (HYALP1), partial sequence
Length = 11957

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Minus

Query: 7 ttactatagggcacgcgtgggtcgacggcccggtg 42
|||||
Sbjct: 11954 ttactatagggcacgcgtgggtcgacggcccggtg 11919

>gi|3643823|gb|AF075270.1|AF075270 Hordeum vulgare high affinity sulfate
transporter (HVST1) gene,
promoter region, 5'UTR, and partial cds
Length = 1094

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtgggtcgacggcccggtg 42
|||||
Sbjct: 64 ttactatagggcacgcgtgggtcgacggcccggtg 99

>gi|19919401|gb|AF435445.1| Pleurotus ostreatus manganese peroxidase (mnp3)
gene, promoter
region and partial cds
Length = 2790

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Plus

Query: 8 tactatagggcacgcgtgggtcgacggcccggtg 42
|||||
Sbjct: 79 tactatagggcacgcgtgggtcgacggcccggtg 113

12/21

>gi|8132114|gb|AF153014.1| Trichomonas vaginalis Tvp14 (tvp14) gene,
complete cds

Length = 1463

Score = 69.9 bits (35), Expect = 6e-09

Identities = 35/35 (100%)

Strand = Plus / Plus

Query: 8 tactatagggcacgcgtggtcgacggcccggtg 42
|||||
Sbjct: 11 tactatagggcacgcgtggtcgacggcccggtg 45

>gi|4456992|gb|AF077743.1|AF077743 Mus musculus transcription factor TFEC
gene, promoter region and

5' UTR

Length = 615

Score = 69.9 bits (35), Expect = 6e-09

Identities = 38/39 (97%)

Strand = Plus / Plus

Query: 9 actatagggcacgcgtggtcgacggcccggtgttatt 47
|||||
Sbjct: 1 actatagggcacgcgtggtcgacggcccggtgttatt 39

>gi|12276207|gb|AF269146.1|AF269146 Bilophila wadsworthia taurine:pyruvate
aminotransferase gene,

complete cds

Length = 2050

Score = 69.9 bits (35), Expect = 6e-09

Identities = 35/35 (100%)

Strand = Plus / Minus

Query: 8 tactatagggcacgcgtggtcgacggcccggtg 42
|||||
Sbjct: 2050 tactatagggcacgcgtggtcgacggcccggtg 2016

>gi|14275833|emb|AJ289605.1|MMU289605 Mus musculus partial Lancl1 gene
for LanC-like protein 1, exon 4

Length = 682

Score = 69.9 bits (35), Expect = 6e-09

Identities = 35/35 (100%)

Strand = Plus / Plus

Query: 9 actatagggcacgcgtggtcgacggcccggtgt 43
|||||
Sbjct: 1 actatagggcacgcgtggtcgacggcccggtgt 35

13/21

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 46 actatagggcacgcgtgggtcgacggcccgggctg 79

>gi|3378604|emb|AJ009889.1|HSAJ9889 Homo sapiens GHR gene, V1 promoter
region
Length = 1640

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctgttatt 47
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctgttatt 39

>gi|3916231|gb|AF074397.1|AF074397 Homo sapiens anti-mullerian hormone type
II receptor (AMHR2)
gene, promoter region and partial cds
Length = 1135

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctgttatt 47
|||||
Sbjct: 13 actatagggcacgcgtgggtcgacggcccgggctgttatt 51

>gi|5139506|emb|Z18892.2|MMDESMINP Mus musculus desmin gene
Length = 19391

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Minus

Query: 8 tactatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 19391 tactatagggcacgcgtgggtcgacggcccgggctg 19357

14/21

>gi|15487305|dbj|AB060299.1| Mus musculus gene for acetyl CoA
synthetase-1, promoter region,
partial sequence
Length = 2094

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctgttatt 47
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctgttatt 39

>gi|12697590|dbj|AB046716.1| Homo sapiens hST3Gal I gene for alpha 2,3-
sialyltransferase I,
promoter region
Length = 1950

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctgttatt 47
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctgttatt 39

>gi|25453365|gb|AY050651.2| Giardia intestinalis MYB (MYB) mRNA, complete
cds
Length = 3069

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 3069 actatagggcacgcgtgggtcgacggcccgggctg 3036

Score = 52.0 bits (26), Expect = 0.001
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 17 gcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 1 gcacgcgtgggtcgacggcccgggctg 26

15/21

>gi|13183059|gb|AF237414.1| Anaplasma phagocytophilum RNA polymerase beta subunit (rpoB) gene,
complete cds
Length = 4185

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 4041 actatagggcacgcgtgggtcgacggcccgggctg 4008

>gi|13625520|gb|AY014277.1| Lolium perenne gibberellin 20-oxidase gene,
complete cds
Length = 2128

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 15 actatagggcacgcgtgggtcgacggcccgggctg 48

>gi|17105179|gb|AF439558.1|AF439558 Mus musculus X2CR1 gene, promoter region and partial cds
Length = 830

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctg 34

>gi|16209547|gb|AY052528.1| Glycine max calmodulin isoform-4 (cam-4) gene, promoter region and partial cds
Length = 2050

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 5 gattactatagggcacgcgtgggtcgacggcccgg 38
|||||
Sbjct: 13 gattactatagggcacgcgtgggtcgacggcccgg 46

16/21

>gi|15213480|gb|AF241535.1|AF241535 Homo sapiens mucin 4 (MUC4) gene,
promoter sequence and partial

cds

Length = 3716

Score = 67.9 bits (34), Expect = 2e-08

Identities = 34/34 (100%)

Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctg 42

|||||

Sbjct: 1 actatagggcacgcgtgggtcgacggccccgggctg 34

>gi|15558849|emb|AJ310936.1|FSO310936 Fusarium solani chy gene for putative
cyanide hydratase enzyme

Length = 1981

Score = 67.9 bits (34), Expect = 2e-08

Identities = 34/34 (100%)

Strand = Plus / Minus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctg 42

|||||

Sbjct: 1981 actatagggcacgcgtgggtcgacggccccgggctg 1948

>gi|4878023|gb|AF131239.2|AF131239 Rattus norvegicus alpha 1,2-
fucosyltransferase C (FTC) gene, complete

cds

Length = 1555

Score = 67.9 bits (34), Expect = 2e-08

Identities = 34/34 (100%)

Strand = Plus / Minus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctg 42

|||||

Sbjct: 1534 actatagggcacgcgtgggtcgacggccccgggctg 1501

>gi|15216031|emb|AJ318812.1|VFA318812 Vicia faba var. minor aapl gene,
promoter region

Length = 1702

Score = 67.9 bits (34), Expect = 2e-08

Identities = 34/34 (100%)

Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctg 42

|||||

Sbjct: 1 actatagggcacgcgtgggtcgacggccccgggctg 34

17/21

>gi|4454294|emb|AJ132779.1|MMU132779 Mus musculus p107 gene promoter region
Length = 776

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctg 34

>gi|3133088|emb|Y16736.1|HSA16736 Homo sapiens dif-2 gene, promoter region
Length = 1368

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 11 actatagggcacgcgtgggtcgacggcccgggctg 44

>gi|6690521|gb|AF154245.1|AF154245 Rattus norvegicus chemotactic protein-3
gene, complete cds
Length = 2416

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctg 34

>gi|5731977|gb|AF114032.1|AF114032 Mus musculus glycogenin-1 gene,
promoter and partial cds
Length = 1958

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
 |||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctg 34

>gi|26453412|dbj|AB094665.1| Seriola quinqueradiata YGHL1 gene for putative
growth hormone
like protein-1, complete cds
Length = 6658

18/21

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtggtcgacggcccgggctg 42
||||||||||||||||||||||||||||||||
Sbjct: 39 actatagggcacgcgtggtcgacggcccgggctg 72

>gi|4039145|gb|AF099083.1|AF099083 Homo sapiens growth hormone secretagogue
receptor gene, 5'
flanking region and partial cds
Length = 1237

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtggtcgacggcccgggctg 42
||||||||||||||||||||||||||||||||
Sbjct: 1 actatagggcacgcgtggtcgacggcccgggctg 34

>gi|2739123|gb|AF029214.1|MMOX2S1 Mus musculus MRC OX-2 antigen homolog
gene, exon 1
Length = 2791

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actatagggcacgcgtggtcgacggcccgggctg 42
||||||||||||||||||||||||||||||||
Sbjct: 2791 actatagggcacgcgtggtcgacggcccgggctg 2758

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtggtcgacggcccgggctg 42
||||||||||||||||||||||||||||||||
Sbjct: 1 actatagggcacgcgtggtcgacggcccgggctg 34

>gi|2895903|gb|AF046916.1|AF046916 Ruminococcus flavefaciens FD-1 glutamine
synthetase type III (glnA)
gene, complete cds
Length = 2685

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

19/21

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 2685 actatagggcacgcgtgggtcgacggcccgggctg 2652

Score = 58.0 bits (29), Expect = 2e-05
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 14 agggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 1 agggcacgcgtgggtcgacggcccgggctg 29

>gi|1916583|gb|U53907.1|RNU53907 Rattus norvegicus microsatellite sequence
D10Mco29
Length = 498

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 5 actatagggcacgcgtgggtcgacggcccgggctg 38

>gi|6683556|dbj|AB024534.1| Rattus norvegicus gene for thiazide-sensitive
Na-Cl
cotransporter, 5' flanking region
Length = 2145.

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggcccgggctg 42
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggcccgggctg 34

>gi|7109286|gb|AF227508.1| Rattus norvegicus intestinal alkaline
phosphatase-II (IAP-II) gene,
complete cds
Length = 6359

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Minus

20/21

Query: 7 ttactatagggcacgcgtgggtcgacggccccggg 39
|||||
Sbjct: 6349 ttactatagggcacgcgtgggtcgacggccccggg 6317

>gi|13345792|gb|AF332759.1| Homo sapiens partially duplicated CHRNA7
gene, hybrid intron A/4
and partial exon 5
Length = 1280

Score = 65.9 bits (33), Expect = 1e-07
Identities = 36/37 (97%)
Strand = Plus / Plus

Query: 11 tatagggcacgcgtgggtcgacggccccgggctgttatt 47
|||||
Sbjct: 8 tatagggcacgcgtgggtcgacggccccgggctgttatt 44

>gi|5002511|emb|Z98266.1|HSZ98266 Homo sapiens gene encoding plakophilin
(exons 1-13)
Length = 49999

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 10 ctatagggcacgcgtgggtcgacggccccgggctg 42
|||||
Sbjct: 16 ctatagggcacgcgtgggtcgacggccccgggctg 48

>gi|6560627|gb|AF112228.1|HSCD30P1 Homo sapiens CD30 protein (CD30) gene,
promoter, partial sequence
Length = 1605

Score = 65.9 bits (33), Expect = 1e-07
Identities = 37/39 (94%)
Strand = Plus / Plus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctgttatt 47
|||||
Sbjct: 1 actatagggcacgcgtgggtcgacggccccgggctgttatt 39

>gi|24475537|dbj|AB084484.1| Betula platyphylla DNA, microsatellite:BpA
Length = 427

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Minus

21/21

Query: 10 ctatagggcacgcgtgggtcgacggccccgggctg 42
|||||
Sbjct: 317 ctatagggcacgcgtgggtcgacggccccgggctg 285

>gi|28875405|gb|AF515463.1| Biomphalaria glabrata fibrinogen related
protein 12.1 precursor
(FREPI2.1) gene, partial cds
Length = 609

Score = 63.9 bits (32), Expect = 4e-07
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 11 tatagggcacgcgtgggtcgacggccccgggctg 42
|||||
Sbjct: 1 tatagggcacgcgtgggtcgacggccccgggctg 32

>gi|18140058|gb|AF457661.1| Castanea dentata clone ACS10A vascular protein
gene, promoter
region
Length = 1157

Score = 63.9 bits (32), Expect = 4e-07
Identities = 35/36 (97%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtgggtcgacggccccgggctg 42
|||||
Sbjct: 10 ttactatagggcacgcgtgggtcgccccgggctg 45

>gi|2581766|gb|U77633.1|RNU77633 Rattus norvegicus chromosome 10
microsatellite D10Mco34
Length = 1023

Score = 63.9 bits (32), Expect = 4e-07
Identities = 33/34 (97%)
Strand = Plus / Minus

Query: 9 actatagggcacgcgtgggtcgacggccccgggctg 42
|||||
Sbjct: 1023 actatagggcacgcvtgggtcgacggccccgggctg 990

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.